

Amendments to the Specification

Please amend the specification as follows:

Please replace the paragraph stating at page 14, line 31 through page 15, line 4, with the following rewritten paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S. F. et al. (1990) J. Mol. Biol. 215: 403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at ~~http://www.ncbi.nlm.nih.gov/BLAST/~~. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively on the internet. ~~at http://www.ncbi.nlm.nih.gov/ncf/bl2.html.~~